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<!--StartFragment-->RESULT 4
ADE08118
ID  ADE08118 standard; protein; 213 AA.
XX
AC  ADE08118;
XX
DT  29-JAN-2004 (first entry)
XX
DE  Novel protein (useful for identifying genetic disorders) #273.
XX
KW  novel gene; novel protein; tissue marker; molecular weight marker;
KW  chromosome marker; genetic disorder.
XX
OS  Unidentified.
XX
PN  WO2003054152-A2.
XX
PD  03-JUL-2003.
XX
PF  10-DEC-2002; 2002WO-US039555.
XX
PR  10-DEC-2001; 2001US-0339739P.
PR  11-DEC-2001; 2001US-0339453P.
PR  14-MAR-2002; 2002US-0365091P.
PR  14-MAR-2002; 2002US-0365384P.
PR  12-APR-2002; 2002US-0372381P.
PR  12-APR-2002; 2002US-0372615P.
PR  22-APR-2002; 2002US-00128558.
PR  24-APR-2002; 2002US-0376045P.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI  Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI  Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR  WPI; 2003-569235/53.
DR  N-PSDB; ADE07207.
XX
PT  New polynucleotides, useful for expressing recombinant proteins for
PT  analysis, characterization or therapeutic use, or as markers for tissues
PT  in which the corresponding protein is preferentially expressed.
XX
PS  Claim 20; SEQ ID NO 1184; 1177pp; English.
XX
CC  The invention comprises the amino acid and coding sequences of novel
CC  proteins. The DNA and protein sequences of the invention are useful as:
CC  markers for tissues in which the corresponding protein is preferentially
CC  expressed; as molecular weight markers on gels; as chromosome markers or
CC  tags; to identify chromosomes or to map related gene positions; and to
CC  compare with endogenous DNA sequences in patients to identify potential
CC  genetic disorders. The present amino acid sequence represents a protein
CC  of the invention.
XX
SQ  Sequence 213 AA;

Query Match          95.1%; Score 1093.5; DB 1; Length 213;
Best Local Similarity 96.2%;
Matches 204; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy          1 MAAASPAF-LRLPLLLLLSSWCRTGLADPHSLCYDITVIPKIRPGPRWCAVQGQVDEKT 59

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Db      1 MAAAASPAFLRLPLLLLLSSWCRTGLADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKT 60
Qy      60 FLHYDCGSKRVTPVSPLGKKLNVTTAWKAQNPNVLREVVDILTEQLLDIQLENYIPKEPLT 119
Db      61 FLHYDCGSKTVPVSPLGKKLNVTTAWKAQNPNVLREVVDILTEQLLDIQLENYIPKEPLT 120
Qy      120 LQARMSCEQKAEGHSGSGWQPSFDGQIFLLFDSQNRMTTTHPGPRKMKEKWENDKDMTM 179
Db      121 LQARMSCEQKAEGHSGSGWQLSFDGQIFLLFDSQNRMTTTHVHGARKMKEKWENDKDMTM 180
Qy      180 SFHYISMGDCTGWLEDFLMGMDSTLEPSAGGT 211
Db      181 SFHYISMGDCTGWLEDFLMGMDSTLEPSAGAT 212
<!--EndFragment-->

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